**Workshop NanoSeq-2017**  
Institute for Integrative Biology of the Cell  
IRS 3D_CHROME  

**Recent Developments with Nanopore Sequencing**  
09 -10 October 2017  
Auditorium IMAGIF  
Building 21, Campus CNRS, Gif-sur-Yvette

**PROGRAM**

**Monday, October 9th 2017**

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
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| 14:00 – 14:15 | Welcome - Short introduction to nanopore sequencing  
Claude Thermes (I2BC, Gif-sur-Yvette)                                      |
| 14:15 – 14:45 | Rapid resistome mapping using nanopore sequencing  
Eric van der Helm (Novo Nordisk Foundation Center for Biosustainability, Denmark) |
| 14:45 – 15:15 | Sequencing and applications using Oxford Nanopore long reads at Genoscope  
Jean-Marc Aury (Genoscope, CEA)                                      |
| 15:15 – 15:45 | Searching for a wild cousin of *Vibrio cholerae*’s secondary chromosome  
François-Xavier Barre (I2BC, Gif-sur-Yvette)                           |
| 15:45 – 16:15 | Coffee break                                                            |
| 16:15 – 16:45 | A precision medicine approach to the diagnosis and management of serious infection using nanopore metagenomic sequencing  
Justin O’Grady (University of East Anglia, Norwich, UK)                  |
| 16:45 – 17:15 | How does the Nanopore technology meet our users’ needs ? Example of the surveillance of Avipoxviruses  
Catherine Zanchetta (GeT-PlaGe - Genotoul, Toulouse)                      |
| 17:15 – 17:45 | Functional dissection of large repetitive transcription units by long read Nanopore sequencing  
Dominik Handler (IMBA, Austria)                                           |

**Tuesday, October 10th 2017**

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<th>Time</th>
<th>Session</th>
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| 9:00 – 9:30   | Lightweight bioinformatics for lightweight sequencing  
Christiaan Henkel (Institute of Biology Leiden, The Netherlands)          |
| 9:30 – 10:00  | Sequencing and assembling plant genomes using Oxford Nanopore long reads  
Benjamin Istace (Genoscope, CEA)                                           |
| 10:00 – 10:30 | Coffee break                                                            |
| 10:30 – 11:00 | Elucidating the expression and splicing patterns of neuropsychiatric disease genes in human brain  
Michael Clark (Garvan Institute of Medical Research, Australia & University of Oxford, UK) |
| 11:00 – 11:30 | Mapping and phasing of structural variations in human genomes using nanopore sequencing  
Wigard Kloosterman (University Medical Center Utrecht, The Netherlands) |
| 11:30 – 12:00 | Genomic and epigenomic classification of cancer using nanopore sequencing  
Philipp Euskirchen (Charité-Universitätsmedizin, Berlin)                  |